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PA	(CORI-) CORIXA CORP.	DR	WPI; 1998-195465/18.
XX	Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;	DR	P-PSDB; AAW56297.
PT	XX	PT	Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid,
XX	DR	PT	vectors transformed cells and antibodies, useful for diagnosis of infection and in protective vaccines
XX	PT	PT	PT
PT	New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient -	PS	PS
XX	XX	PS	Claim 1: Page 96; 118pp; English.
PS	Claim 1: Page 96; 118pp; English.	XX	The sequence is that encoding a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using: (a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
XX	XX	XX	XX
XX	Sequence 1460 BP: 539 A; 252 C; 283 G; 386 T; 0 other;	SQ	Sequence 1820 BP; 402 A; 398 C; 334 G; 686 T; 0 other;
XX	XX	XX	XX
XX	Alignment Scores:	Alignment Scores:	Alignment Scores:
XX	Pred. No. : 2.97e-13	Length: 1460	Length: 1820
Score: 139.00	Matches: 26	Score: 139.00	Matches: 1820
Percent Similarity: 100.00%	Conservative: 0	Percent Similarity: 100.00%	Conservative: 26
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0	Query Match: 100.00%	Indels: 0
DB: 21	Gaps: 0	DB: 19	Gaps: 0
US-09-794-764-195 (1-26) x AAC65100 (1-1460)		US-09-794-764-195 (1-26) x AAV22747 (1-1820)	
QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20		QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20	
Db 1287 GCAACCCATAAGCAATAAGCTGAGCTGAAGAAATCGCATGATCTCAGACA 1346		Db 793 GGCAACCCATAAGCAATAAGCTGAGCTGAAGAAATCGCATGATCTCAGACA 734	
QY 21 ThrGlnGluLysCysGlu 26		QY 21 ThrGlnGluLysCysGlu 26	
Db 1347 ACGCAAGAAATATGCAA 1364		Db 733 ACGCAAGAAATATGCAA 716	
RESULT 4		RESULT 5	
AAV22747/C		AAV22753	
ID AAV22747 standard; DNA; 1820, BP.		ID AAV22753 standard; DNA; 1820 BP.	
AC AAV22747;		AC AAV22753;	
XX DT 28-SEP-1998 (first entry)		XX AC AAV22753;	
XX DE Babesia microti BMNI-17 antigen sequence.		XX DT 28-SEP-1998 (first entry)	
XX KW antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis; ss.		XX DE Babesia microti BMNI-17 antigen complement sequence.	
XX OS Babesia microti.		XX KW antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis; ss.	
XX FH Key Location/Qualifiers		XX OS Babesia microti.	
FT CDS 98 . 832		XX FH Key	
FT FT /*tag= a		FT CDS complement (98 . 832)	
XX PN EP834567-A2.		FT FT /*tag= a	
XX PD 08-APR-1998.		FT FT /product= antigen	
XX PD 01-OCT-1997; 97EP-0117067.		XX PN EP834567-A2.	
XX PR 24-APR-1997; 97US-0845258.		XX PD 08-APR-1998.	
PR 01-OCT-1996; 96US-0723142.		XX PR 01-OCT-1997; 97EP-0117067.	
XX (CORI-) CORIXA CORP.		XX PR 24-APR-1997; 97US-0845258.	
PA Houghton R, Lodes MJ, Reed SG, Sleath PR;		XX PR 01-OCT-1996; 96US-0723142.	
PI (CORI-) CORIXA CORP.		PA (CORI-) CORIXA CORP.	



CC The present invention describes isolated polypeptides comprising  
 CC specific immunogenic portions of Babesia microti. AAC88983 to AAC88994  
 CC encode specifically claimed B. microti immunogenic proteins, and  
 CC AA124327 to AAY24338 represent these proteins. B. microti polypeptides  
 CC and nucleic acids can be used for detecting B. microti infections. They  
 CC can also be used in vaccines for inducing protective immunity against B.  
 CC microti infections. The present sequence encodes B. microti antigen.  
 XX

Sequence 1820 BP: 686 A; 334 C; 398 G; 402 T; 0 other;

Alignment Scores:

Pred. No.: 3.89e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US-09-794-764-195 (1-26) x AAC65094 (1-1820)

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 1 GlyLYSProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 Percent Similarity: 100.00% Matches: 139.00  
 Best Local Similarity: 100.00% Conservative: 139.00  
 Query Match: 100.00% Mismatches: 0  
 DB: 793 GGCACAAACCAATAGGATAAAAAGGATGAAAGGCTGAAAGAAAATGCCATGATCTAGACA 734  
 XX

US-09-794-764-195 (1-26) x AAC890012 (1-1820)

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

RESULT 9

AAC65095  
 ID AAC65095 standard; DNA; 1820 BP.  
 XX  
 AC AAC65095;  
 XX DT 12-FEB-2001 (first entry)  
 XX DE B. microti BMNI-17 antigen reverse complement SEQ ID NO: 37.  
 XX KW Babesiosis; rodent parasite; tick-borne illness; antigen;  
 XX disease diagnosis; disease prevention; ds.  
 XX OS Babesia microti.  
 XX PN WO200060090-A1.  
 XX PR 05-APR-2000; 2000WO-US09136.  
 XX PD 12-OCT-2000.  
 XX PF 05-APR-1999; 99US-0286488.  
 XX PR 17-MAR-2000; 2000US-0528784.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;  
 XX PS Example 1; Page 86; 118pp; English.  
 XX DR The present invention is related to the isolation of antigenic sequences  
 CC from the rodent parasite Babesia microti. This organism is transmitted to  
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.  
 CC The organism causes a malaria-like infection known as babesiosis. The  
 CC sequences identified by this invention can be used in the diagnosis,  
 CC prevention and treatment of babesiosis.

XX SQ Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-794-764-195 (1-26) x AAC65094 (1-1820)

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

Alignment Scores:  
 Pred. No.: 1.39e-13 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

XX The present invention is related to the isolation of antigenic sequences  
 CC from the rodent parasite Babesia microti. This organism is transmitted to  
 CC humans by the same tick which transmits Lyme disease and ehrlichiosis.  
 CC The organism causes a malaria-like infection known as babesiosis. The  
 CC sequences identified by this invention can be used in the diagnosis,  
 CC prevention and treatment of babesiosis.

XX SQ Sequence 1820 BP; 686 A; 334 C; 398 G; 402 T; 0 other;

US-09-794-764-195 (1-26) x AAC65095 (1-1820)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
DB 1028 GGAAACCCAAATAGAATAAAAGTGAAGGGCTGAAAGAAATCGATCTAGACA 1087

QY 21 ThrGlnGluLleCysGlu 26  
DB 1088 ACCGCAAGAAATATCTGAA 1105

RESULT 10  
ID AAC65119 standard; cDNA; 2001 BP.  
XX DT 12-FEB-2001 (first entry)

B. microti MN-10/BMNI-17 fusion protein cDNA SEQ ID NO: 84 .

XX DE 05-APR-1999; 9905-0286488.  
XX PR 17-MAR-2000; 2000US-0528784.  
XX PA (CORI-) CORIXA CORP.

XX PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;  
XX PD 12-OCT-2000.  
XX PF 05-APR-2000; 2000WO-US09136.  
XX PR 05-APR-1999; 9905-0286488.  
XX PA (CORI-) CORIXA CORP.

XX PS Example 5; Page 108; 118pp; English.  
XX DR 2000-686939/67.

XX PT New polypeptides containing an antigenic portion of Babesia microti  
XX antigen and DNAs encoding the polypeptides, useful for diagnosing,  
XX treating or preventing B. microti infection, or for inducing protective  
XX immunity in a patient -

XX PS Example 5; Page 111-112; 118pp; English.  
XX DR 2000-686939/67.

XX PT The present invention is related to the isolation of antigenic sequences  
CC from the rodent parasite Babesia microti. This organism is transmitted to  
CC humans by the same tick which transmits Lyme disease and ehrlichiosis.  
CC The organism causes a malaria-like infection known as babesiosis. The  
CC sequences identified by this invention can be used in the diagnosis,  
CC prevention and treatment of babesiosis.

XX SQ Sequence 2001 BP; 742 A; 334 C; 462 G; 463 T; 0 other;  
XX

Alignment Scores:  
Pred. No.: 4.37e-13 Length: 2001  
Score: 139.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 GlnGluLleCysGlu 26

US-09-794-764-195 (1-26) x AAC65119 (1-2001)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
DB 1207 GGAAACCCAAATAGAATAAAAGTGAAGGGCTGAAAGAAATCGATCTAGACA 1266

QY 21 ThrGlnGluLleCysGlu 26  
DB 12-FEB-2001 (first entry)

Db 1267 ACGCAAGAAATATCTGAA 1284  
RESULT 11  
ID AAC65120 standard; cDNA; 3402 BP.  
XX AC AAC65120;  
XX DT 12-FEB-2001 (first entry)  
DE B. microti MN-10/BMNI-17/BMNI-15 fusion protein cDNA SEQ ID NO: 86 .  
XX KW Babesiosis; rodent parasite; tick-borne illness; antigen;  
XX disease diagnosis; disease prevention; ss.  
XX OS Babesia sp.  
XX PN WO200060090-A1.  
XX PR 12-OCT-2000.  
XX PD 05-APR-2000; 2000WO-US09136.  
XX PF 05-APR-1999; 99US-0286488.  
XX PR 17-MAR-2000; 2000US-0528784.  
XX PA (CORI-) CORIXA CORP.

XX PI Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD;  
XX DR 2000-686939/67.

XX PT New polypeptides containing an antigenic portion of Babesia microti  
XX antigen and DNAs encoding the polypeptides, useful for diagnosing,  
XX treating or preventing B. microti infection, or for inducing protective  
XX immunity in a patient -

XX PS Example 5; Page 111-112; 118pp; English.  
XX DR 2000-686939/67.

XX PT The present invention is related to the isolation of antigenic sequences  
CC from the rodent parasite Babesia microti. This organism is transmitted to  
CC humans by the same tick which transmits Lyme disease and ehrlichiosis.  
CC The organism causes a malaria-like infection known as babesiosis. The  
CC sequences identified by this invention can be used in the diagnosis,  
CC prevention and treatment of babesiosis.

XX SQ Sequence 3402 BP; 1184 A; 615 C; 712 G; 891 T; 0 other;  
XX

Alignment Scores:  
Pred. No.: 8.41e-13 Length: 3402  
Score: 139.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 ThrGlnGluLleCysGlu 26

US-09-794-764-195 (1-26) x AAC65120 (1-3402)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
DB 2605 GGAAACCCAAATAGAATAAAAGTGAAGGGCTGAAAGAAATCGATCTAGACA 2664

QY 21 ThrGlnGluLleCysGlu 26  
DB 2665 ACGCAAGAAATATCTGAA 2682  
RESULT 12  
ID ABL15763 standard; cDNA; 1760 BP.  
XX AC ABL15763;  
XX DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41771.  
 DE XX  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 KW XX  
 XX WO200171042-A2.  
 XX  
 OS Drosophila melanogaster.  
 OS XX  
 PN WO200171042-A2.  
 XX  
 XX PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 XX DR 2001-656800/75.  
 DR P-PSDB; ABB71650.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1; SEQ ID NO 41768; 21pp + Sequence Listing; English.  
 PS  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL0511, expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABL57737-ABL72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).  
 CC  
 XX Sequence 1760 BP; 476 A; 405 C; 490 G; 389 T; 0 other;  
 XX  
 SQ Alignment Scores:  
 Pred. No.: 11.9 Length: 1760  
 Score: 57.00 Matches: 12  
 Percent Similarity: 58.33% Conservative: 2  
 Best Local Similarity: 50.00% Mismatches: 10  
 Query Match: 41.01% Indels: 0  
 DB: 23 Gaps: 0  
 US-09-794-764-195 (1-26) x ABL15762 (1-6725)  
 Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 Db 287 GCGGGTCAAATACAAAAAGCGAAAAGGAATCAATTACAGTAGTGGTCAAACAGTACTGCTCAACAAACG 346  
 Qy 21 ThrGlnGluL 24  
 Db 347 GCCCCAGGAAGTC 358  
 RESULT 13  
 ABL15762/C ID ABL15762 standard; cDNA; 6725 BP.  
 XX  
 AC ABL15762;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41768  
 DE Drosophila; developmental biology; cell signalling; insecticide;  
 KW KW  
 KW cytosine methylation; ds.  
 XX  
 OS Homo sapiens.

XX WO200168912-A2.  
 XX 20-SEP-2001.  
 XX 15-MAR-2001; 2001WO-EP02955.  
 XX 15-MAR-2000; 2000DE-1013847.  
 PR 06-APR-2000; 2000DE-1019058.  
 PR 07-APR-2000; 2000DE-1019173.  
 PR 30-JUN-2000; 2000DE-103259.  
 PR 01-SEP-2000; 2000DE-1043826.  
 XX PA (EPIG ) EPIGENOMICS AG.  
 XX PI Olek A, Piepenbrock C, Berlin K;  
 XX DR WPI; 2001-602752/68.  
 XX PR Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer -  
 XX PS Claim 1; SEQ ID No 164; 27pp; English.  
 XX The invention relates to a nucleic acid comprising a sequence of 18 bases of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (ss). The nucleic acid may be a peptide nucleic acid-oligonucleotide (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing).  
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX Sequence 6200 BP; 1487 A; 134 C; 1522 G; 3057 T; 0 other;  
 XX SO Alignment Scores:  
 Pred. No.: 81.7 Length: 6200  
 Score: 56.00 Matches: 11  
 Percent Similarity: 60.00% Conservative: 1  
 Best Local Similarity: 55.00% Mismatches: 8  
 Query Match: 40.29% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-794-764-195 (1-26) x ABL09172 (1-31449)  
 Pred. No.: 729 Length: 31449  
 Score: 55.50 Matches: 12  
 Percent Similarity: 65.22% Conservative: 3  
 Best Local Similarity: 52.17% Mismatches: 7  
 Query Match: 39.93% Indels: 1  
 DB: 23 Gaps: 1  
 US-09-794-764-195 (1-26) x ABL09172 (1-6200)  
 QY 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrGln 22  
 DB 29046 CCGAACACATAAAAGTAAAAAAACGAAACGTACTCGCACAGCACACAAACTACGCC 1172  
 RESULT 15  
 ABL09172/C  
 ID ABL09172 standard; cDNA; 31449 BP.  
 XX Search completed: October 12, 2002, 20:55:49  
 Job time : 183 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2002, 18:42:28 ; search time 18:33 Seconds  
(without alignments)  
296,830 Million cell updates/sec

Title: US-09-794-764-195  
Perfect score: 139

Sequence: 1 GRPNTNKEAKRKSHTDTQTTICE 26

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Dgapop 6.0 , Delext 7.0

Searched: 179656 seqs, 1046268233 residues

Total number of hits satisfying chosen Parameters:

3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n,model -DEV=1,h  
-O=/cgn2\_1/JUSP10\_spool/US09794764/runat\_12102002\_184217\_5216/app-query.fasta\_1.199  
-DB=GenEmbl -QPI=0 -PREFIX=rge -MNIMATCH=0.1 -LOOPEXT=0  
-UNITS=bites -SPART=1 -END=1 -MATRIX=b1000sum62 -TRANS=human40\_cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE\_Pt -THE\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTENV=plot -NORM=ext -HEAPSIZ=2500 -MINLEN=0 -MAXLEN=1000000000  
-USER=US09794764 @CGN 1.11773 @runat\_12102002\_184217\_5216 -NCPU=6 -ICPU=3  
-NO\_XLPPX -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMBOUT=30 -THREADS=1 -XGAPOF=10 -XGAPST=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DEL05=6 -DELEXT=7

GenEmbl: \*

1: gb\_ba: \*  
2: gb\_hg: \*  
3: gb\_in: \*  
4: gb\_on: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pi: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_num: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_p1: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*

29: em\_vt: \*  
30: em\_hg\_hum: \*  
31: em\_hg\_inv: \*  
32: em\_hg\_other: \*  
33: em\_hg\_oInv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	139	100.0	1460	3	AF206527	Babesia m
2	139	100.0	1460	6	AR129329	Sequence
3	139	100.0	1460	6	AX304537	Sequence
4	139	100.0	1820	3	AF206526	Babesia m
5	139	100.0	1820	6	AR129323	Sequence
6	139	100.0	1820	6	AR129324	Sequence
7	139	100.0	1820	6	AR173458	Sequence
8	139	100.0	1820	6	AR173459	Sequence
9	139	100.0	1820	6	AX304533	Sequence
10	139	100.0	1820	6	AX304523	Sequence
11	139	100.0	2050	6	AX304510	Sequence
12	139	100.0	2034	6	AX304629	Sequence
13	139	100.0	2079	6	AX304696	Sequence
14	139	100.0	3405	6	AX304572	Sequence
15	68	48.9	20094	2	AC220862	Mus muscu
16	61	43.9	212637	2	AL662919	Mus muscu
17	61	43.9	223957	2	AL645993	Mus muscu
18	60.5	43.5	26977	3	CEP40F8	269302 Caenorhabid
19	60	43.2	5929	9	AL445163	Human DNA
20	60	43.2	14433	2	AC07962	Rattus no
21	59	42.4	6371	2	AC100417	Mus muscu
22	58.5	42.1	112484	2	AC103259	Rattus no
23	58	41.7	141271	2	AL133304	Homo sapi
24	58	41.7	167979	2	AL354770	Homo sapi
25	57	41.0	9220	3	AC029651	Ac029551 Giardia i
26	57	41.0	2243	3	AV011256	Drosophila
27	57	41.0	2243	3	DM30603	Drosophila
28	57	41.0	6405	14	AF020051	Blackcurr
29	57	41.0	16706	2	AC015093	Drosophila
30	57	41.0	10500	9	AP002988	Homo sapi
31	57	41.0	11300	8	AC087192	Oryza sat
32	57	41.0	13936	9	HS003834	
33	57	41.0	17193	2	AC021438	
34	57	41.0	179316	3	AC022351	Drosophila
35	57	41.0	223750	2	AC073750	Mus muscu
36	57	41.0	23924	2	AC079569	
37	57	41.0	30180	3	AE003502	Drosophili
38	56.5	40.6	15436	2	AP011387	Homo sapi
39	56.5	40.6	155847	9	AC090415	
40	56.5	40.6	172693	2	AC074246	Homo sapi
41	56.5	40.6	296820	10	AF31233	Mus muscu
42	56	40.3	1048	11	CNS06K1Y	AL402332 T3 end of
43	56	40.3	2827	8	SCMDJ1P	z28336 S.cerevisia
44	56	40.3	4527	14	U79033	U79033 Kilham rat
45	56	40.3	6200	6	AX251196	AX251196 Sequence

## ALIGNMENTS

RESULT 1  
AF206527  
DOCUS Babesia microti strain MN1 seroreactive antigen BMN1-20 gene,  
DEFINITION partial cds.  
ACCESSION AF206527  
VERSION AF206527.1  
KEYWORDS GT:7716018  
SOURCE Babesia microti.

ORGANISM	Babesia microti Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;	source	1. 1460 /organism="unknown" BASE COUNT 539 a	252 c	283 g	386 t
REFERENCE	1 (bases 1 to 1460)	BASE COUNT	539 a	252 c	283 g	386 t
AUTHORS	Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R., Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.	ORIGIN				
TITLE	Serological expression cloning of novel immunoreactive antigens of Babesia microti.	Alignment Scores:	5.55e-12	Length:	1460	
JOURNAL	Infect. Immun. 68 (5), 2783-2790 (2000).	Pred. No.:	139.00	Matches:	26	
MEDLINE	20231818	Score:	100.00%	Conservative:	0	
POEMED	10768973	Percent Similarity:	100.00%	Mismatches:	0	
REFERENCE	2 (bases 1 to 1460)	Best Local Similarity:	100.00%	Indels:	0	
AUTHORS	Lodes, M.J., Houghton, R.L., Bruinsma, E.S., Mohamath, R., Reynolds, L.D., Benson, D.R., Krause, P.J., Reed, S.G. and Persing, D.H.	Query Match:	100.00%	Gaps:	0	
TITLE	Direct Submission	DB:	6			
JOURNAL	Submitted (18-NOV-1999) Corixa Corporation, 1124 Columbia Street, Suite 200, Seattle, WA 98104, USA	US-09-794-764-195 (1-26) x AR129329 (1-1460)				
FEATURES	Location/Qualifiers	QY	1 GlyLysProAsnThrAsnLysSerGluArgLysSerHisAspThrGlnThr 20			
source	1 - 1460 /organism="Babesia microti" /strain="MNI" /db_xref="taxon:5868"	Db	1287 GGCAAACCCATAACGAAATAACGAAATGAGAAAGCTGAAAGAAAATCCGATCTAGAGACA 1346			
sig_peptide	636 . 701 /note="predicted cleavable signal sequence"	QY	21 ThrGlnGluLysCysGlu 26			
CDSS	636 . >1460 /note="putative secreted protein"	Db	1347 ACGCAAGAAATATGTGAA 1364			
	/function="unknown"	RESULT 3				
	/codon_start=1 /product="secreted protein BMN1-20"	AX304537	1460 bp	DNA	linear	PAT 30-NOV-2001
	/protein_id="AAF68455.1" /db_xref="GI:17116019"	LOCUS	AX304537			
	/translation="MVNULSPGILLISAYSINSASAGDYYEISSGNPPDIEPTSTSL TNNVNTYIPEPNADSESVSEVQIHDNINPQDADSEPIEQMPSDTRVLPESDGV HOFRLGHISMDASDINDEPAPWEDAPYFSDDEELDNLMLRLTAQ ETSDSDHHERGKLNNTKSEKTERKSHDQTPOQYEFLDNLLATQELYERKEGH KPNPNKSEAEKSHDQTPOQYEFLDNLLATQELYERKEGH Db_xref="taxon:5868"	DEFINITION	Sequence 51 from Patent WO0185947.			
		ACCESSION	AX304537			
		VERSION	AX304537.1			
		KEYWORDS	GI:17383870			
		SOURCE	Babesia microti.			
		ORGANISM	Babesia microti.			
		COMMENT	Babesia microti.			
		REFERENCE	Babesia.			
		AUTHORS	1 (sites) Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D.			
		JOURNAL	Corixa Corporation (US)			
		FEATURES	Location/Qualifiers			
		SOURCE	Homer, M.J. and Sechrist, H.			
		TITLE	Compounds and methods for the diagnosis and treatment of Babesia			
		COMMENT	microti infection			
		REFERENCE	Patent: WO 0185947-A 51 15-NOV-2001;			
		AUTHORS	CORIXA CORPORATION (US)			
		JOURNAL				
		FEATURES				
		SOURCE				
		TITLE				
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		REFERENCE				
		AUTHORS				
		JOURNAL</td				



QY 1 GlyylsProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 DB 1028 GCGAACCCAAATAGCAATAAAAGCTGAAAGCTGAAATGCTGATCATCTAGACAA 1087

QY 21 ThrGlnGluLysCysGlu 26  
 DB 1088 ACGCAAGAAATATGTGAA 1105

RESULT 7  
 AR173458/c LOCUS AR173458 1820 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 17 from patent US 6306396.  
 ACCESSION AR173458  
 VERSION AR173458..1 GI:17913778  
 KEYWORDS Unknown.  
 SOURCE Unclassified.  
 ORGANISM Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.  
 REFERENCE Title Compounds and methods for the diagnosis and treatment of *B. microti* infection  
 AUTHORS Patent: US 6306396-A 17 23-OCT-2001;  
 TITLE 1..1820 /organism="unknown"  
 JOURNAL Location/Qualifiers  
 FEATURES Source  
 BASE COUNT 402 a 398 c 334 g 686 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7e-12 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent. Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x AR173458 (1-1820)

QY 1 GlyylsProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 DB 793 GCGAACCCAAATAGCAATAAAAGCTGAAAGAAATGCTGATCATCTAGACAA 734

QY 21 ThrGlnGluLysCysGlu 26  
 DB 733 ACGCAAGAAATATGTGAA 716

RESULT 8  
 AR173459 LOCUS AR173459 1820 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 37 from patent US 6306396.  
 ACCESSION AR173459  
 VERSION AR173459..1 GI:17913779  
 KEYWORDS Unknown.  
 SOURCE Unclassified.  
 ORGANISM Reed, S.G., Lodes, M.J., Houghton, R. and Sleath, P.R.  
 REFERENCE Title Compounds and methods for the diagnosis and treatment of *B. microti* infection  
 AUTHORS Patent: US 6306396-A 37 23-OCT-2001;  
 TITLE 1..1820 /organism="unknown"  
 JOURNAL Location/Qualifiers  
 FEATURES Source  
 BASE COUNT 686 a 398 c 398 g 402 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7e-12 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent. Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 DB: 0 Gaps: 0

US-09-794-764-195 (1-26) x AR173459 (1-1820)

QY 1 GlyylsProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 DB 1028 GCGAACCCAAATAGCAATAAAAGCTGAAAGAAATGCTGATCATCTAGACAA 1087

QY 21 ThrGlnGluLysCysGlu 26  
 DB 1088 ACGCAAGAAATATGTGAA 1105

RESULT 9  
 AX304503/c LOCUS AX304503 1820 bp DNA linear PAT 30-NOV-2001  
 DEFINITION Sequence 17 from Patent WO0185947.  
 ACCESSION AX304503  
 VERSION AX304503..1 GI:17383864  
 KEYWORDS Babesia microti.  
 SOURCE Babesia microti.  
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasida; Babesiidae;  
 Babesia.  
 REFERENCE Authors Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D., Homer, M.J. and Sechrist, H.  
 TITLE Compounds and methods for the diagnosis and treatment of *Babesia microti* infection  
 JOURNAL Patent: WO 0185947-A-17 15-NOV-2001;  
 FEATURES Location/Qualifiers  
 BASE COUNT 402 a 398 c 334 g 686 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 7e-12 Length: 1820  
 Score: 139.00 Matches: 26  
 Percent. Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US-09-794-764-195 (1-26) x AX304503 (1-1820)

QY 1 GlyylsProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 DB 793 GCGAACCCAAATAGCAATAAAAGCTGAAAGAAATGCTGATCATCTAGACAA 734

QY 21 ThrGlnGluLysCysGlu 26  
 DB 733 ACGCAAGAAATATGTGAA 716

RESULT 10  
 AX304523 LOCUS AX304523 1820 bp DNA linear PAT 30-NOV-2001  
 DEFINITION Sequence 37 from Patent WO0185947.  
 ACCESSION AX304523  
 VERSION AX304523..1 GI:17383865  
 KEYWORDS Babesia microti.  
 SOURCE Babesia microti.  
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Piroplasida; Babesiidae;  
 Babesia.  
 REFERENCE Authors Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D., Homer, M.J. and Sechrist, H.  
 TITLE Compounds and methods for the diagnosis and treatment of *Babesia microti* infection  
 JOURNAL Patent: WO 0185947-A 37 15-NOV-2001;

FEATURES	CORIXA CORPORATION (US)	ACCESSION	AX304629
source	Location/Qualifiers	VERSION	AX304629.1
1. .1820		KEYWORDS	Gr:17383934
/organism="Babesia microti"		SOURCE	Babesia sp.
BASE COUNT	686 a	ORGANISM	Babesia sp.
ORIGIN	334 c	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;	Babesia.
Alignment Scores:		REFERENCE	
Pred. No. : 7e-12	Length: 1820	AUTHORS	Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D.,
Score: 139.00	Matches: 26	TITLE	Homer, M.J. and Secrist, H.
Percent. Similarity: 100.00%	Conservative: 0	Compounds and methods for the diagnosis and treatment of Babesia	
Best Local Similarity: 100.00%	Mismatches: 0	JOURNAL	Patent: WO 0185947-A 143 15-NOV-2001;
Query Match: 100.00%	Indels: 0	CORIXA CORPORATION (US)	
DB: 6	Gaps: 0	FEATURES	Location/Qualifiers
US-09-794-764-195 (1-26) x AX304523 (1-1820)		source	1. .2034
Qy 21 GlyLysProAsnThrAsnLysSerGluLysSerHisAspThrGlnThr 20		/organism="Babesia sp."	
Db 1028 GGCAAACCCATAAGAAATAAGGAGAGCTAAAGAAATCGCATATCTCAGACA 1087		/db_xref="taxon:35084"	
RESULT 11		BASE COUNT	746 a
LOCUS AX304570	Sequence 84 from Patent WO0185947.	ORIGIN	343 c
DEFINITION AX304570	2001 bp	FEATURES	472 g
ACCESSION AX304570.1	DNA	source	473 t
VERSION GI:17383889	linear		
KEYWORDS	PAT 30-NOV-2001		
REFERENCE 1. (sites)		US-09-794-764-195 (1-26) x AX304629 (1-2034)	
AUTHORS Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D.,		Qy 1 GlyLysProAsnThrAsnLysSerGluLysSerHisAspThrGlnThr 20	
TITLE Homer, M.J. and Secrist, H.		Db 523 GGCAAACCCATAAGGATATAAGTGAAGGGCTGAAGAAAATCGCATGTACTCAGACA 582	
JOURNAL Compounds and methods for the diagnosis and treatment of Babesia		Qy 21 ThrGlnGluLysCysLys 26	
Patent: WO 0185947-A 84 15-NOV-2001;		Db 583 ACGCAAGAAATATGCAA 600	
FEATURES CORIXA CORPORATION (US)		RESULT 13	
source 1. .2001	Location/Qualifiers	LOCUS AX304696	AX304696
BASE COUNT 742 a	/organism="Babesia sp."	DEFINITION Sequence 210 from Patent WO0185947.	DNA
ORIGIN 334 c	/db_xref="taxon:35084"	ACCESSION AX304696	1
Alignment Scores:		VERSION AX304696.1	GR:17383965
Pred. No. : 7.74e-12	Length: 2001	KEYWORDS	Babesia microti.
Score: 139.00	Matches: 26	SOURCE	Babesia microti.
Percent. Similarity: 100.00%	Conservative: 0	ORGANISM	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
Best Local Similarity: 100.00%	Mismatches: 0	REFERENCE	Babesia.
Query Match: 100.00%	Indels: 0	AUTHORS	Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., Mcneill, P.D.,
DB: 6	Gaps: 0	TITLE	Homer, M.J. and Secrist, H.
US-09-794-764-195 (1-26) x AX304570 (1-2001)		Compounds and methods for the diagnosis and treatment of Babesia	
Qy 21 ThrcGlnGluLysCysGlu 26		JOURNAL	Patent: WO 0185947-A 210 15-NOV-2001;
Db 1267 AGCGAAGAAATATGCAA 1284		CORIXA CORPORATION (US)	
RESULT 12		FEATURES	Location/Qualifiers
LOCUS AX304629	Sequence 143 from Patent WO0185947.	source	1. .2079
DEFINITION	2034 bp	/organism="Babesia microti"	
BASE COUNT 782 a	DNA	/db_xref="taxon:5868"	
ORIGIN 354 c	linear	US-09-794-764-195 (1-26) x AX304696 (1-2079)	
Alignment Scores:		Alignment Scores:	
Pred. No. : 8.06e-12	Length: 2079	Pred. No. :	8.06e-12
Score: 139.00	Matches: 26	Score:	139.00
Percent. Similarity: 100.00%	Conservative: 0	Percent. Similarity:	100.00%
Best Local Similarity: 100.00%	Mismatches: 0	Best Local Similarity:	100.00%
Query Match: 100.00%	Indels: 0	Query Match:	100.00%
DB: 6	Gaps: 0	DB:	6
Qy 21 ThrcGlnGluLysCysGlu 26		BASE COUNT	422 g
Db 1207 GGCAAACCCATAAGAAACTGAGAGCTGAAGAAAATCGCATGATACTCAGACA 1266		ORIGIN	521 t

QY	1	GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr	20	COMMENT	On Mar 29, 2000 this sequence version replaced gi:6686446.
Db	1287	GGCAAACCCAAATACGAAATAAAAGTGAAGGGCTGAAAGAAAATCGATCATCTAGACA	1346	Center	Joint Genome Institute
QY	21	ThrGlnGluLysCysGlu	26	Center Code:	JGI
Db	1347	ACGCAAGAAATAATGTGAA	1364	Web site:	<a href="http://www.jgi.doe.gov">http://www.jgi.doe.gov</a>
RESULT	14			-----	Summary Statistics
AC	AX304572			Consensus quality:	131468 bases at least Q40
LOCUS	AX304572	3402 bp	DNA	Consensus quality:	161121 bases at least Q30
DEFINITION	Sequence 86 from Patent WO0185947.			Consensus quality:	172522 bases at least Q20
ACCESSION	AX304572			Estimated insert size:	200054: sum-of-contigs estimation
VERSION	AX304572.1	GI:17383890		Estimated insert size:	194000: pulse field gel estimation
KEYWORDS				Quality coverage:	3.14x in Q20 bases; pulse field gel estimation
ORGANISM	Babesia sp.			Quality coverage:	3.05x in Q20 bases; sum-of-contigs estimation
REFERENCE	Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., McNeill, P.D., Homer, M.J. and Secrist, H.			-----	-----
AUTHORS				* NOTE: This is a 'working draft' sequence. It currently	
TITLE	Compounds and methods for the diagnosis and treatment of Babesia			* consists of 52 contigs. The true order of the pieces	
DEFINITION	microt in fection			* is not known and their order in this sequence record	
JOURNAL	Patent: WO 0185947-A 86 15 NOV-2001;			* is arbitrary. Gaps between the contigs are represented as	
ACCESSION	CORIXA CORPORATION (US)			* runs of N, but the exact sizes of the gaps are unknown.	
VERSION	1. .3402			* This record will be updated with the finished sequence	
KEYWORDS				* as soon as it is available and the accession number will	
ORGANISM	Babesia sp.			* be preserved.	
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;			1 1123: contig of 1123 bp in length	
AUTHORS	Babesia.			* 1 1124: gap of unknown length	
TITLE	1 (sites)			* 1 1124: contig of 1357 bp in length	
DEFINITION	Reed, S.G., Lodes, M.J., Houghton, R.L., Sleath, P.R., McNeill, P.D., Homer, M.J. and Secrist, H.			* 1 1124: contig of 1209 bp in length	
JOURNAL	Compounds and methods for the diagnosis and treatment of Babesia			* 1 1124: contig of 1278 bp in length	
ACCESSION	microt in fection			* 1 1124: contig of 1030 bp in length	
VERSION	Patent: WO 0185947-A 86 15 NOV-2001;			* 1 1124: contig of 1352 bp in length	
KEYWORDS	CORIXA CORPORATION (US)			* 1 1124: contig of 1483 bp in length	
REFERENCE	Location/Qualifiers			* 1 1124: contig of 1047 bp in length	
AUTHORS	1. .3402			* 1 1124: contig of 1306 bp in length	
TITLE	/organism="Babesia sp."			* 1 1124: contig of 1285 bp in length	
DEFINITION	/db_xref="taxon:3084"			* 1 1124: contig of 1446 bp in length	
JOURNAL	BASE COUNT	1184	a	* 1 1124: contig of 1720 bp in length	
ACCESSION	615	c	712	* 1 1124: contig of 1295 bp in length	
VERSION	g	891	t	* 1 1124: contig of 1445 bp in length	
KEYWORDS				* 1 1124: contig of 1970 bp in length	
ORGANISM	ORIGIN			* 1 1124: contig of 1682 bp in length	
REFERENCE				* 1 1124: contig of 1516 bp in length	
AUTHORS				* 1 1124: contig of 1825 bp in length	
TITLE				* 1 1124: contig of 1761 bp in length	
DEFINITION				* 1 1124: contig of 1189 bp in length	
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 Job time : 1845 secs

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**	42986	contig of 1455 bp in length	
**	42987	gap of unknown length	
**	44994	contig of 1968 bp in length	
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**	50900	gap of unknown length	
**	54324	contig of 2008 bp in length	
**	54325	gap of unknown length	
**	58499	contig of 2726 bp in length	
**	62290	gap of unknown length	
**	62291	contig of 3180 bp in length	
**	67699	gap of unknown length	
**	67700	contig of 3424 bp in length	
**	72720	gap of unknown length	
**	78607	contig of 4174 bp in length	
**	85624	gap of unknown length	
**	85625	contig of 4792 bp in length	
**	92161	gap of unknown length	
**	98562	contig of 5020 bp in length	
**	105679	gap of unknown length	
**	111169	contig of 5887 bp in length	
**	119079	gap of unknown length	
**	119080	contig of 6401 bp in length	
**	128004	gap of unknown length	
**	134622	contig of 6536 bp in length	
**	142335	gap of unknown length	
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Db 47997 GGAGGACAGATAACAGAAAAGCAAGAAACACACACACACAAAGA 47938			

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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2002, 18:42:28 ; Search time 39 Seconds  
(without alignments)  
163.756 Million cell updates/sec

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Perfect score: 139  
Sequence: 1 GKPNTNKSEKAERKSHDTQITQEICE 26

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Ygapop 10.0 ; Ygapext 0.5  
Fgapop 6.0 ; Fgapext 7.0  
Dgapop 6.0 ; Delext 7.0

Searched: 385533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPCCL=0 -UNITS=bits -START=1 -END=1 -MATRIX=100sun62 -TRANS=human40.cdi
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a printed score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	139	100.0	1460	4	US-09-845-258-51	Sequence 51, Appl
2	139	100.0	1460	4	US-09-90-571-51	Sequence 51, Appl
c 3	139	100.0	1820	4	US-09-845-258-37	Sequence 37, Appl
c 4	139	100.0	1820	4	US-09-845-258-37	Sequence 37, Appl
c 5	139	100.0	1820	4	US-09-90-571-17	Sequence 17, Appl
c 6	139	100.0	1820	4	US-09-90-571-37	Sequence 17, Appl
c 7	139	100.0	1820	4	US-09-873-142A-17	Sequence 17, Appl
c 8	139	100.0	1820	4	US-09-873-142A-37	Sequence 37, Appl
9	54	38.8	43676	3	US-09-356-952-12	Sequence 12, Appl
10	48	34.5	6755	3	US-08-931-999-4	Sequence 4, Appl
11	47	33.8	634	2	US-08-222-719-15	Sequence 15, Appl
12	47	33.8	634	2	US-08-471-613-15	Sequence 15, Appl
					PCT-US92-0105-15	Sequence 6, Appl
					US-08-941-349-6	Sequence 3, Appl
					US-08-841-349-3	Sequence 14, Appl
					US-08-423-383-14	Sequence 14, Appl
					US-08-437-353A-14	Sequence 8, Appl
					US-09-160-8	Sequence 1, Appl
					PCT-US92-0105-1	Sequence 12, Appl
					US-09-185-160-12	Sequence 5, Appl
					US-08-503-172-5	Sequence 5, Appl
					US-09-135-211-5	Sequence 5, Appl
					US-08-972-927-5	Sequence 5, Appl
					US-08-996-621-1	Sequence 1, Appl
					US-08-905-223-199	Sequence 199, Appl
					US-09-188-930-205	Sequence 210, Appl
					US-09-188-930-205	Sequence 205, Appl
					US-09-188-930-41	Sequence 41, Appl
					US-09-172-841-52	Sequence 52, Appl
					US-08-794-216-2	Sequence 2, Appl
					US-08-073-384C-2	Sequence 2, Appl
					US-09-590-020-3	Sequence 3, Appl
					US-09-590-020-5	Sequence 5, Appl
					US-08-254-359A-2	Sequence 2, Appl
					US-08-481-043-2	Sequence 2, Appl
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					US-08-184-956-2	Sequence 2, Appl
					US-08-577-653-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1 ; Sequence 51, Application US/08845258-51  
; Patent No. 6183976  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Sleath, Paul R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08-845-258  
; FILING DATE: 24-APR-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121-426C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 51:

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SEQUENCE CHARACTERISTICS:
; LENGTH: 1460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE: Babesia Microti
; US-08-845-258-51

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US-09-794-764-195 (1-26) x US-08-990-571-51 (1-1460)

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RESULT 3
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Sequence 17, Application US/08845258
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; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,258
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121-426C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE: Babesia Microti
; US-08-990-571-51

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Score: 139.00 Matches: 26
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Query Match: 4 Indels: 0
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US-09-794-764-195 (1-26) x US-08-845-258-17 (1-1820)

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QY 21 ThrGlnGluLysCysGlu 26

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 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Loeches, Michael J.  
 ; APPLICANT: Houghton, Raymond  
 ; APPLICANT: Sleath, Paul R.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS  
 ; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. MICOTI INFECTION  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/845,258  
 ; FILING DATE: 24-APR-1997  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Maki, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.426C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-1900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 37:  
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 ; LENGTH: 1820 base pairs  
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 ; STRANDEDNESS: single  
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 ; US-08-845-258-37

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 US-08-990-571-17/C  
 ; Sequence 17, Application US/0890571  
 ; Patent No. 6214971  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G. et al.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.  
 ; NUMBER OF SEQUENCES: 79  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/990,571  
 FILING DATE: 11-DEC-1997  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:

RESULT 6

Db 793 GGCAAAACCCATAACGATAAAAGTGGAAAGGCTGAAAGAAATCGATGACTCAGACA 734  
 Qy 21 ThrGlnGluLileCysGlu 26  
 Db 733 ACGCAAGAAATATGCAA 716  
 US-08-990-571-37  
 ; Sequence 37, Application US/0890571  
 ; Patent No. 6214971  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G. et al.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.  
 ; NUMBER OF SEQUENCES: 79  
 ; CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED AND BERRY  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/990,571  
 FILING DATE: 11-DEC-1997  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:

```

; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-990-571-37

Alignment Scores:
Pred. No.: 5.74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-794-764-195 (1-26) x US-08-723-142A-17 (1-1820)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GGCAAAACCCATACCAATAAAGTGAAGGAAATCCATGTAACGTACTGAGACA 734

RESULT 8
US-08-723-142A-37
; Sequence 37, Application US/08723142A
; Patent No. 6306396
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF B. MICRIDI INFECTION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08-723-142A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-723-142A-37

Alignment Scores:
Pred. No.: 5.74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-794-764-195 (1-26) x US-08-723-142A-37 (1-1820)

; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-990-571-37

Alignment Scores:
Pred. No.: 5.74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-794-764-195 (1-26) x US-08-723-142A-17 (1-1820)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20
Db 793 GGCAAAACCCATACCAATAAAGTGAAGGAAATCCATGTAACGTACTGAGACA 734

RESULT 7
US-08-723-142A-17/C
; Sequence 17, Application US/08723142A
; Patent No. 6306396
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF B. MICRIDI INFECTION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08-723-142A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.426
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-723-142A-37

Alignment Scores:
Pred. No.: 5.74e-15 Length: 1820
Score: 139.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-794-764-195 (1-26) x US-08-723-142A-37 (1-1820)

```

**RESULT 9**  
 S-09-356-952-12  
 Sequence 12, Application US/09356652  
 Patent No. 6117653  
 GENERAL INFORMATION:  
 APPLICANT: Borlack-Sjodin, Ann  
 APPLICANT: Margarit, S. M.  
 APPLICANT: Bor-Sogi, Da-Fna  
 APPLICANT: Cole, Phillip  
 APPLICANT: Kurian, John  
 TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE  
 TITLE OF INVENTION: THEREOF  
 FILE REFERENCE: 600-1-28N  
 CURRENT APPLICATION NUMBER: US/09/356,952  
 CURRENT FILING DATE: 1999-07-19  
 EARLIER APPLICATION NUMBER: 60/093,631  
 EARLIER FILING DATE: 1998-07-24  
 NUMBER OF SEQ ID NOS: 14  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 12  
 LENGTH: 43676  
 TYPE: DNA  
 ORGANISM: *Saccharomyces cerevisiae*

3. PROGRESSIVE ALIGNMENT OF THE SEQUENCES  
 Alignment Scores : 43676  
 Aligned No. : 278  
 Score: 54.00  
 Exacent Similarity: 70.00%  
 Least Local Similarity: 45.00%  
 Every Match: 38.85%  
 BPs: 3  
 Length: 43676  
 Matches: 9  
 Conservative: 5  
 Mismatches: 6  
 Indels: 0  
 Gaps: 0  
 S-09-794-764-195 (1-26) x US-09-356-952-12 (1-43676)

APPLICANT: Iandolo, John J.  
APPLICANT: Crupper, Scott S.  
TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hovey, Williams, Timmons & Collins  
CITY: Boston, MA  
STATE: MA  
ZIP: 02116

SITE: 2405 Grand Boulevard, Suite 400  
CITY: Kansas City  
STATE: Missouri  
COUNTRY: U.S.A.  
ZIP: 64108

COMPUTER READABLE FORM:

    MEDIUM TYPE: Floppy disk  
    COMPUTER: IBM PC compatible  
    OPERATING SYSTEM: PC-DOS/MS-DOS  
    SOFTWARE: Patentin Release #1.0, Version #1.30  
    CURRENT APPLICATION DATA:  
        APPLICATION NUMBER: US/08/1931,999  
        FILING DATE:  
        CLASSIFICATION: 514  
        PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Collins, John M.
  REGISTRATION NUMBER: 26,262
  REFERENCE/DOCKET NUMBER: 25043-A
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 816/474-9050
  TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
  LENGTH: 6755 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: unknown
  MOLECULE TYPE: DNA (genomic)
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
ORIGINAL SOURCE:
  ORGANISM: Staphylococcus aureus
  STRAIN: UT0007
US-08-931-999-4

Alignment Scores:
  Pred No.: 267
  Score: 48.00
  Percent Similarity: 76.47%
  Best Local Similarity: 47.06%
  Query Match: 34.53%
  DB: 3

  Len:
  Ma:
  Co:
  Mi:
  In:
  Ga:
  Len-00-794-76A-105 / 1-261 x US-08-931-000

```

NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,719  
FILING DATE: 04-April-1994  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,136  
FILING DATE: 30-October-1992  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 07/86/229001  
TELECOMMUNICATION INFORMATION



Alignment Scores:  
 Pred. No.: 17.8  
 Score: 47.00  
 Percent Similarity: 54.17%  
 Best Local Similarity: 37.50%  
 Query Match: 33.81%  
 DB: 2

US-09-794-764-195 (1-26) x US-08-471-61-3-15 (1-634)

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 Db 274 GGAAGGAAGGTACTGCACCATCTGAAACTAAGCTGAATGGTAAACTAAAGCTGAAGGCAAGAAA 333

Qy 21 ThrGlnGluLle 24  
 Db 334 ACTGAATCTCTA 345

RESULT 14  
 PCT-US93-10443-15  
 Sequence 15, Application PC/TUS9310443  
 GENERAL INFORMATION:  
 APPLICANT: David D. Moore  
 APPLICANT: Jae W. Lee  
 TITLE OF INVENTION: NUCLEAR HORMONE RECEPTOR-  
 TITLE OF INVENTION: INTERACTING POLYPEPTIDES AND  
 TITLE OF INVENTION: RELATED MOLECULES AND METHODS  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 CITY: 225 Franklin Street  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM PS/2 Model 50Z or 55SX  
 OPERATING SYSTEM: MS-DOS (version 5.0)  
 SOFTWARE: Wordperfect (version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/10443  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 07/969,136  
 FILING DATE: October 30, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Paul T. Clark  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00786/099002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELELEX: 200154  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 634  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 PCT-US93-10443-15

Qy 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 Db 274 GGAAGGAAGGTACTGCACCATCTGAAACTAAGCTGAATGGTAAACTAAAGCTGAAGGCAAGAAA 333

Qy 21 ThrGlnGluLle 24  
 Db 334 ACTGAATCTCTA 345

RESULT 15  
 US-08-841-349-6  
 Sequence 6, Application US/08841349B  
 Patent No. 5555594  
 GENERAL INFORMATION:  
 APPLICANT: MISHRA, LOPA  
 TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT  
 FILE REFERENCE: XX/PO4470US0  
 CURRENT APPLICATION NUMBER: US/08/841,349B  
 CURRENT FILING DATE: 1997-04-30  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 6  
 LENGTH: 1312  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (402)..(1061)  
 US-08-841-349-6

Alignment Scores:  
 Pred. No.: 46.3  
 Score: 47.00  
 Percent Similarity: 58.33%  
 Best Local Similarity: 37.50%  
 Query Match: 33.81%  
 DB: 2

US-09-794-764-195 (1-26) x US-08-841-349-6 (1-1312)

Qy 3 ProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThrThrGln 22  
 Db 873 CCAAACAGCAAGGTTCAGGGAGCTCAAGGATCTCAAATGGGATCTCAAAGGAGAC 932

Qy 23 GluIleCysGlu 26  
 Db 933 CAAGTTCCCAAG 944

Search completed: October 12, 2002, 21:23:19  
 Job time : 42 secs

Alignment Scores:  
 Pred. No.: 17.8  
 Score: 47.00  
 Percent Similarity: 54.17%  
 Best Local Similarity: 37.50%  
 Query Match: 33.81%  
 DB: 5

US-09-794-764-195 (1-26) x PCT-US3-10443-15 (1-634)

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Result No.	Score	Query	Match Length	DB ID	Description	8
1	63	45.3	453	12	A0615735	A0615735 HS_5143_A
2	60.5	43.5	771	10	B1J24088	B1J24088 A

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2002, 18:42:27 ; Search time 1584 Seconds  
(without alignment) 221.541 Million cell updates/sec

Title: US-09-794-764-195

Perfect score: 139

Sequence: 1 GKPNTNKSBEAKRKSHDITQTQICE 26

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEVP=xiH  
-Q=/cgn2\_1/USPRO/spool -SUFFIX=xrsl -MINMATCH=0.1 -LOOPCFL=0 -LOOPEXT=0  
-DB=EST -QPMT=fastop -START=1 -END=1 -UNITS=bits -MATRIX=blosum62 -TRANS=human40\_cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pot -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFILE=pt0 -NORM=ext -HEAPSIZE=500 -MINLEN=2000000000  
-USER=US09-794-764\_@CGN\_1..1144\_@runat\_12102002\_184218\_5229 -NCPU=6 -ICPU=3  
-NO\_XLDPY -NO\_MMAP -LARGEQUER -NEG\_SCORES=0 -WAIT -LONGLOG -DEV -TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST : \* EST : \*

1: em\_estba:\*

2: em\_estbm:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: qb\_est1:\*

10: qb\_est2:\*

11: qb\_hcc:\*

12: qb\_gss:\*

13: em\_gss\_hm:\*

14: em\_gss\_iny:\*

15: em\_gss\_pln:\*

16: em\_gss\_vrt:\*

RESULT 1

AQ615735

LOCUS HS\_5143\_A2\_E06\_SP6E\_RPCI-11\_Human

DEFINITION genomic\_clone\_Plate-719

REFERENCE 1 (bases 1 to 453)

AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and

Hood, L.

VERSION 0615735.1

ACCESSION AQ615735.1

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Library Homo sapiens

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

High throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

#### SUMMARIES

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Email: jwallace@washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm)) or from Research Genetics (<http://www.resgen.com>). BAC end Web Server: <http://www.htsc.washington.edu>  
 Plate: 719 row: I column: 12  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 453.

FEATURES	source	Location/Qualifiers
	1. .453	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="Plate=719 Col=12 Row=I" /clone_lib="RPCI-11 Human Male BAC Library" /sex="male" /note="Vector: PBACE3 6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the PBACE3 6 vector at EcoRI sites"
BASE COUNT	158 a 112 c 109 g 68 t 6 others	
ORIGIN		
Alignment Scores:		
pred. No.:	36.8	Length: 453
Score:	63.00	Matches: 14
Percent Similarity:	68.00%	Conservative: 3
Best Local Similarity:	56.00%	Mismatches: 6
Query Match:	45.32%	Indels: 2
DB:	12	Gaps: 1
US-09-794-764-195 (1-26) x AQ615735 (1-453)		
Qy 1 GlyLysProAsnThrAspLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20		
Db 330 GGTAAACCCAAAGGCAATAAAAGTTGAGGCGCCAGCGAAAATCC-----ACCCAAAAAC 383		
Qy 21 ThrGlnGluIleCys 25		
Db 384 ACGGGGAGATATGTC 398		
RESULT 2		
LOCUS	BJ124088	771 bp mRNA linear EST 23-JAN-2000
DEFINITION	BJ124088 unpublished oligo-capped cDNA library, C. elegans L1 stage	
ACCESSION	BJ124088	
VERSION	BJ124088.1 GI:18284228	
KEYWORDS	Caenorhabditis elegans	
SOURCE	Caenorhabditis elegans	
ORGANISM	Caenorhabditis elegans Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides; Rhabditidae; Peloderrinae; Caenorhabditis.	
REFERENCE	1. (bases 1 to 771)	
AUTHORS	Kohara, Y., Shin, I., T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y., and Sugano, S.	
TITLE	A complementary view of the C. elegans genome	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Tadasu Shin-1 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp.	
FEATURES	Location/Qualifiers	
source	1. .771 /organism="Caenorhabditis elegans" /strain="N2" /substrain="N2-53200"	

Percent Similarity:	70.83%	Conservative:	4	RESULT	5
Best Local Similarity:	54.17%	Mismatches:	2	AZ015973	477 bp
Query Match:	43.53%	Indels:	5	RPCI-23-290C2	DNA
DB:	10	Gaps:	1	TJ	linear
US-09-794-764-195 (1-26) x BG121328 (1-1321)				RPCI-23	Mus musculus genomic clone RPCI-23-290C2,
Qy 4 AsnThrAsnLysserGluLysAlaGluArgLysSerHis-----AspThr 18					
Db 1014 AACACCAACAGACAGAGAAACAAACAGAAAGAACA 1073					
Qy 19 GlnThrThrGln 22					
Db 1074 CAAACCAACAG 1085					
RESULT 4 AW698464/c					
LOCUS AW698464	390 bp	mRNA	linear	EST	17-APR-2000
DEFINITION 9419 glandular-haired subtracted cDNA library <i>Medicago sativa</i> cDNA, mRNA sequence.					
ACCESSION AW698464					
VERSION AW698464.1	GI:7581050				
EST.					
ORGANISM <i>Medicago sativa</i>					
SOURCE <i>Medicago sativa</i>					
Medicagaceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.					
REFERENCE 1 (bases 1 to 390)					
AUTHORS Hays, D. and Skinner, D.					
TITLE Expressed sequence tags subtracted in reciprocal fashion between glandular-haired and non-glandular-haired full sibs of <i>alfalfa</i>					
JOURNAL Unpublished (2000)					
COMMENT Contact: Hays DB					
USDA, ARS, GMRC, PSERU, Department of Agronomy					
Kansas State University					
Throckmorton Hall, Manhattan, KS 66506, USA					
Tel: 785 532 7116					
Fax: 785 532 6167					
Email: dhays@esys.alfalfa.ksu.edu					
Seq primer: SP6.					
FEATURES source					
Location/Qualifiers 1. 390					
/organism="Medicago sativa"					
/cultivar="Riley X KS224"					
/db_xref="taxon:3873"					
/clone_lib="glandular-haired subtracted cDNA library"					
/tissue_type="Leaf and stem"					
/note="glandular-haired versus non-glandular-haired reciprocal cDNA subtraction with CLONTECH PCR-Select cDNA subtraction."					
BASE COUNT 107 a 101 c 74 g 108 t					
ORIGIN					
Alignment Scores:					
Pred. No.:	79.5	Length:	390	Length:	477
Score:	60.00	Matches:	12	Matches:	13
Percent Similarity:	73.91%	Conservative:	5	Percent Similarity:	62.9%
Best Local Similarity:	52.17%	Mismatches:	6	Best Local Similarity:	48.15%
Query Match:	43.17%	Indels:	0	Query Match:	42.45%
DB:	9	Gaps:		DB:	12
US-09-794-764-195 (1-26) x AW698464 (1-390)					
Qy 3 proAsnThrAsnLysserGluLysAlaGluArgLysSerHisaspThrGlnThrGln 22					
Db 384 CCATGGTTAACAAAAGCCCCAACGAAACCTAGAGTCATCTGTCACATATGAA 325					
Qy 23 GluIleCys 25					
Db 324 CAAATCTGT 316					
RESULT 6					

DEFINITION	BF216649 707 bp mRNA linear EST 06-NOV-2000 Homo sapiens IMAGE:4095539 5', mRNA sequence.	KEYWORDS	EST. human.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 763)	REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS	NIH-MGC	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	NIH-MGC	TITLE	Unpublished (1999)
JOURNAL		JOURNAL	Unpublished (1999)
COMMENT	COMMENT	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@mail.nih.gov
FEATURES	source	FEATURES	Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov/Plate: LICM1795 row: e column: 02
source	source	source	High quality sequence stop: 541. Location/Qualifiers
source	1. 707	source	1. 763 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4095539" /clone_id="NIH_MGC_57" /tissue_type="glioblastoma" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: muscle; Vector: pORB7; Site_1: SfiI (ggccatttggcc); Site_2: SfiI (ggccatttggcc); Site_1: SfiI (ggccccctccggcc); Site_2: SfiI (ggccatttggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5', adaptor sequence: 5'-ATTCGAGCGCGAGCGACATG-3' (30) BN-3', sequence: 5'-ATTCGAGCGCGAGCGAGCGACATG-3' (30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
source	225 a 154 c 237 g 91 t	source	BASE COUNT 237 a 209 c 186 g 131 t ORIGIN
source	211	source	Alignment Scores: Pred. No.: 230 Score: 59.00 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0 DB: 0
source	59.00	source	Length: 763 Matches: 11 Conservative: 59.00 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	72.73%	source	Length: 763 Matches: 11 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	45.45%	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	42.45%	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	10	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	21	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	22	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	692	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
source	687	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
RESULT	7	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
LOCUS	BF825967	source	Length: 763 Matches: 10 Conservative: 6 Percent Similarity: 72.73% Best Local Similarity: 50.00% Query Match: 42.45% DB: 10 DB: 0
DEFINITION	BF825967 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4900969 5', mRNA sequence.	DEFINITION	338 bp mRNA full-length enriched, 10 days neonate cortex Mus
ACCESSION	BF825967	ACCESSION	BB274997 RIKEN cDNA clone A830090118 3', mRNA sequence.
VERSION	BF825967.1	VERSION	BB274997.1 GI:8972018
RESULT	7	RESULT	EST. house mouse.
LOCUS	BF825967	LOCUS	Mus musculus
DEFINITION	BF825967 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4900969 5', mRNA sequence.	DEFINITION	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ACCESSION	BF825967	ACCESSION	BB274997 (bases 1 to 338)
VERSION	BF825967.1	VERSION	BB274997
REFERENCE	REFERENCE	REFERENCE	Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Itoh, M.,







KEYWORDS EST, human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;  
 Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1300)  
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contract: Robert Strausberg, Ph.D.  
 COMMENT Email: [capbs@mail.nih.gov](mailto:capbs@mail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LUCM1759 row: h column: 19  
 High quality sequence stop: 94.

FEATURES source  
 Location/Qualifiers 1. 1300  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4876482"  
 /clone\_lib="NIH\_MGC\_43"  
 /tissue\_type="normal Pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; vector: pORB7; Site\_1: XbaI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XbaI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH-MGC Library. 1" 35 t

BASE COUNT 576 a 293 c 396 g 35 t  
 ORIGIN

Alignment Scores: Pred. No.: 569 Length: 1300  
 Score: 58.00 Matches: 1.0  
 Percent Similarity: 73.91% Conservative: 7  
 Best Local Similarity: 43.48% Mismatches: 6  
 Query Match: 41.73% Indels: 0  
 DB: 10 Gaps: 0

US-09-794-764-195 (1-26) x BI608655 (1-238)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 DB 1212 CGAAAACCAGGACGCGAACGGAGAACGCGAACGGAAACACGAAACGCAAAGC 1271  
 QY 21 ThrGlnGlu 23  
 DB 1272 AGAAAAAA 1280

RESULT 15  
 BI608655  
 LOCUS BI608655\_1  
 DEFINITION RH13261\_5 prime RH Drosophila melanogaster mRNA  
 Drosophila melanogaster cDNA clone RH13261 5, mRNA sequence.  
 ACCESSION BI608655  
 VERSION EST  
 KEYWORDS EST, Drosophila melanogaster  
 SOURCE fruit fly.  
 ORGANISM Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta;  
 Pterygota: Neoptera: Endopterygota; Diptera: Brachycera;  
 Muscomorpha: Ephydioidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 238)  
 REFERENCE Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson  
 , J., Chame, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George

TITLE BDGP/HMMI RH Drosophila EST Project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Stapleton, M.  
 BDGP  
 Lawrence Berkeley National Lab  
 One Cyclotron Rd, Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
 Plate: RH 132 row: F column: 1  
 High quality sequence stop: 235.  
 Location/Qualifiers 1. 238  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone="RH13261"  
 /clone\_lib="RH Drosophila melanogaster normalized head  
 pFLC-1"  
 /sex="male and female"  
 /dev\_stage="Adult"  
 /lab\_host="DH5-alpha TonA"  
 /note="Organ: head; Vector: pFLC1; Site\_1: XbaI; Site\_2:  
 BamH1; Library was kindly generated by Piero Carninci at  
 the RIKEN. The library was normalized and excised using  
 Cre recombinase. Plasmid cDNA library."  
 BASE COUNT 81 a 47 c 61 g 48 t 1 others  
 ORIGIN

Alignment Scores: Pred. No.: 117 Length: 238  
 Score: 57.00 Matches: 12  
 Percent Similarity: 58.33% Conservative: 2  
 Best Local Similarity: 50.00% Mismatches: 10  
 Query Match: 41.01% Indels: 0  
 DB: 10 Gaps: 0

US-09-794-764-195 (1-26) x BI608655 (1-238)

QY 1 GlyLysProAsnThrAsnLysSerGluLysAlaGluArgLysSerHisAspThrGlnThr 20  
 DB 51 GCGGGCICCAANTACAAAAGGGAAATCAATTACAGTAGTGCTCAACAAACG 110  
 QY 21 ThrGlnGlu 24  
 DB 111 GCCCAGGAAGTC 122

Search completed: October 12, 2002, 21:22:28  
 Job time : 1589 secs